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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2996.72 Seconds
(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-10
Perfect score: 1164
Sequence: 1 atgaagtccacgttgctat.....caggttgcgaagaagtaa 1164

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
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5: gb.ov.*
6: gb.pat.*
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41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	251.6	21.6	840	3	AB045172
2	246.8	21.2	828	3	AB045179
3	244.2	21.0	730	3	AB045168
4	241.8	20.8	808	3	AB045178
5	240.6	20.7	710	3	AB045171
6	232.4	20.1	774	3	AB045170
7	232.8	20.0	781	3	AB045165
8	231	19.8	784	3	AB045167
9	227.8	19.6	798	3	AB045166
10	221.4	19.0	1443	8	FSOKCH
11	221.4	19.0	1473	6	A21795
12	221.4	19.0	1473	6	A23637
13	221.4	19.0	1473	6	A23646
14	221.4	19.0	1473	6	A23955
15	221.4	19.0	1473	6	A23959
16	221.4	19.0	1473	6	A41660
17	221.4	19.0	1473	6	AR072922
18	221.4	19.0	1473	6	BD002249
19	221.4	19.0	1473	6	BD010853
20	221.4	19.0	1473	6	I13885
21	221.4	19.0	1473	6	I21317
22	221.4	19.0	1473	6	I57984
23	217.4	18.7	761	3	AB045175
24	213.6	18.4	785	3	AB045169
25	212.2	18.2	759	3	AB045174
26	212.2	18.2	802	3	AB045176
27	211.8	18.2	783	3	AB045173
28	210.6	18.1	785	3	AB045177
29	207.4	17.8	1423	6	AR094309
30	204	17.5	912	6	A68076
31	204	17.5	912	6	AR163170
32	202.8	17.4	919	6	A68072
33	202.8	17.4	919	6	AR163168
34	200.6	17.2	924	6	A68074
35	200.6	17.2	924	6	AR163169
36	188	16.2	922	6	A68078
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38	186.8	16.0	922	6	A68070
39	186.8	16.0	922	6	AR163167
40	186	16.0	1154	6	AR094308
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42	184	15.8	1174	6	AR075389
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44	179.4	15.4	1057	6	BD002248
45	179.4	15.4	1060	6	A21793

ALIGNMENTS

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LOCUS
DEFINITION
AB045172
Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
cellulase homologue, clone:8-44, complete cds.
ACCESSION
AB045172
VERSION
AB045172.1
KEYWORDS
GI:5926976
SOURCE
Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
clone:8-44.
ORGANISM
Reticulitermes speratus hindgut symbiont 130484
Unclassified.
REFERENCE
1 (sites)
AUTHORS
Ohmoto,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE
Diverse genes of cellulase homologues of glycosyl hydrolase family

45 from the symbiotic protists in the hindgut of the termite
Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)
21020023
2 (bases 1 to 840)
Ohkuma, M.
Direct Submission
Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
Physical and Chemical Research), Microbiology Laboratory; Hirose
2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
Fax:66-48-462-4672)
Location/Qualifiers
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Best Local Similarity 65.4%; Pred. No. 3e-55;
Matches 403; Conservative 0; Mismatches 204; Indels 9; Gaps 2;
QY 555 TGGTTCACCAACTCGTTATGGAGTGTGTAAGCTTCTTGACGCTGGCTGGAAAGC 614
DB 78 TGGGAGGACCACCGCTTACTGGACTGTGTGAAAGCTTCGTGTGCATGGGAAAAAAGC 137
QY 615 TTCTGTCACTGTCTGTGTGACACCTGTGCCTCCAAATGGTATCTTTATTAG-----A 668
DB 138 TCGTGTGACTAGCTGTGTGACATGCGCAAGATGGCAACACGAGTGTGAAGCAA 197
QY 669 TCCCAATGCTCAAGTGGTGTGTAACGGTGGTAAGTGTTCATGTGTAAACAACCAACC 728
DB 198 TCACACAGTGAATCTTGTGTGTGTGATGGAGGAGATACATGTGTATGATCAAGCACC 257
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QY 789 CGAAGCTGGATGTTGTGTGTGTGTATGAATGACCTTCACTTCTGCGCTGTCTTGG 848
DB 315 CGAAGCGGTGTTGTGTAATGCTATGAGCTTACCTTCAACAGTGGCCAGTTAATGG 374
QY 849 AAGAAGATGTTGTTCAAGATTACCAACACCGTGGCGATTTAGGCTCTAACCACTTTGA 908
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QY 909 TTTGCAATCCCGGTGGTGGCGTGTGTATCTTCAATGGCTGTGCTGCTCAATGGGGCGC 968
DB 435 TCTTGCAATTTCCGGAGGAGGTGTGCGAATTTACATGGATGCACTCAACAATCAGGGGC 494
QY 969 TCCCAATGATGGTGGGAGCTAGATATGTTGTGTGCTGCTGTCTGCTGCTGCTGCTC 1028
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QY 1149 TTGCGAAAGAAAGTAA 1164
DB 675 TTGCAAGCGAAGTAA 690
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LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
DEFINITION cellulase homologue, clone:6-47, complete cds.
ACCESSION AB045179
VERSION AB045179.1 GI:8926990
KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
SOURCE clone:6-47.
ORGANISM Reticulitermes speratus hindgut symbiont 130484
Unclassified.
REFERENCE 1 (sites)
AUTHORS Ohkuma, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family
45 from the symbiotic protists in the hindgut of the termite
Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)
JOURNAL MEDLINE 21020023
REFERENCE 2 (bases 1 to 828)
AUTHORS Ohkuma, M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
Physical and Chemical Research), Microbiology Laboratory; Hirose
2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
Fax:66-48-462-4672)
Location/Qualifiers
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Query Match 21.2%; Score 246.8; DB 3; Length 828;
Best Local Similarity 64.9%; Pred. No. 5.5e-54;
Matches 400; Conservative 0; Mismatches 207; Indels 9; Gaps 2;
QY 555 TGGTTCACCAACTCGTTATGGAGTGTGTAAGCTTCTTGACGCTGGCTGGAAAGC 614
DB 79 TGGGAGGACTACCGTGTATTTGGGATTTGTTGCAAGCGTTCATGTGCAATGGAAGAAAGC 138
QY 615 TTCTGTCACTGTGCTGTGTCACACCTGTGCTCCAATGGTATCTCTTTATTAG-----A 668
DB 139 TCGTGTGACTACCGCTGTGATGATGCTGTGGAAGATGGGACAAAGACTTCAAGCAA 198
QY 669 TGCCCAATGCTCAAGTGGTGTAAACGGTGGTAAATGTTTCACTGTGTAAACAACCAACC 728
DB 199 TGACACAGTAAATCGAGTTGTGTATGCGGAGATGGATACATGTGTATGATCAAGCACC 258
QY 729 TTGGGCTGTCAATGATGAGCTCGCTTACGGTTTTCGCTGCTGCTCTATTCTGCTGCCAA 788
DB 259 ATGGGCTGTAAATGACTCAGTTGCTATGTTTGGAGCTGCAGCTTGTCTGTGG---AGG 315
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Db 316 TGAGACTGGAGCTTGTTCGAATTGCTATGAGCTTACGTTCCAGAGTGGCCAGTGAATGG 375

QY 849 AAGAAGATGGTGTTCACAGTTACCAACACCGGTGGGATTTTAGGCTCTAAACACATTTGA 908

Db 376 AAGAAGATGGTGTTCACAGTTACCAACACCGGTGGGATTTTAGGCTCTAAACACATTTGA 435

QY 909 TTTGCAAAATGCCCGGTGGTGGCTTGTATCTTCAATGGCTGTGCTCAATGGGGCGC 968

Db 436 TCTTGCAAATTCACAGGAGGAGTGTGGAAATTTACAAATGGATGCACTCAGCAATCAGGTGC 495

QY 969 TCCCAATGATGGCTGGGAGCTAGATATGGTGTGCTCAGCTCTGTCTGACTGTGCTCCTC 1028

Db 496 ACCTGCTGATGGATGGGAGCGCTTATGGTGTGTGTCATCTGCTTCTGAATGTTCTCA 555

QY 1029 TCTTCCCTCTGCTCTTCAAGCTGTTGTAATGGAGATTCAACTGGTTCAAGAACTCTGA 1088

Db 556 ACTTCTTCTGCTCTTCAAGCTGTTGTAATGGAGATTCAACTGGTTCAAGAACTCTGA 615

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Db 616 CAACCTTCAATCAATTTCAACCAAGTAGACATGCCCAAGTGAATTTGATAGCAAGAACAA 675

QY 1149 TTGCGAAAGAACTAA 1164

Db 676 TTGCAAAACGTACTTAA 691

RESULT 3

AB045168 780 bp mRNA linear INV 14-FEB-2001

LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45

DEFINITION cellulase homologue, clone:4-44, complete cds.

ACCESSION AB045168

VERSION AB045168.1 GI:8926968

KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cdna to mRNA, clone:4-44.

SOURCE Reticulitermes speratus hindgut symbiont 130484

ORGANISM Unclassified.

REFERENCE 1 (sites)

AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.

TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus

JOURNAL Extremophiles 4 (6), 343-349 (2000)

MEDLINE 2102023

REFERENCE 2 (bases 1 to 780)

AUTHORS Ohkuma,M.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosewa 2-1, Wako-shi, Saitama 351-0198, Japan

(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)

FEATURES

source Location/Qualifiers

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Query Match 21.0%; Score 244.2; DB 3; Length 780;

Best Local Similarity 64.4%; Pred. No. 2.6e-53;

Matches 401; Conservative 0; Mismatches 213; Indels 9; Gaps 2;

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Db 304 GGAGGTGAGAA-SCCTGCCCTGCTGTAAT---TGTACGAGTTGACTTTCACCTCTGGCCCC 360

QY 841 GCTTCTTGGAAAGATGGTGTTCAGATTACCAACACCGGTGGCGATTTAGGCTCTAAC 900

Db 361 GTTAATGGCAAGATGACTGTTCAAGGTTTACCAACACCGGAGGTGATCTCGGTTTCAAT 420

QY 901 CACTTTGATTTCGCAATGCCCGTGGTGGCTTGTATCTTCAATGGCTGTGCTGCTCAA 960

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QY 1141 CGCTCAGGTTGCGAAAGAAAGTA 1163

Db 661 AAAACCAATTGCAGCGCAATTA 683

RESULT 4

AB045178 808 bp mRNA linear INV 14-FEB-2001

LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45

DEFINITION cellulase homologue, clone:45-6, complete cds.

ACCESSION AB045178

VERSION AB045178.1 GI:8926988

KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cdna to mRNA, clone:45-6

SOURCE Reticulitermes speratus hindgut symbiont 130484

ORGANISM Unclassified.

REFERENCE 1 (sites)

AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.

TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus

JOURNAL Extremophiles 4 (6), 343-349 (2000)

MEDLINE 2102023

REFERENCE 2 (bases 1 to 808)

AUTHORS Ohkuma,M.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosewa 2-1, Wako-shi, Saitama 351-0198, Japan

(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,

FEATURES
source
CDS

AB045171.1 GI:8926974
Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
clone:7-50.
Reticulitermes speratus hindgut symbiont 130484
Unclassified.

ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

1. (sites)
Ohtoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
Diverse genes of cellulase homologues of glycosyl hydrolase family
45 from the symbiotic protists in the hindgut of the termite
Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)
21020023
2. (bases 1 to 710)
Ohkuma, M.
Direct Submission
Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
Physical and Chemical Research), Microbiology Laboratory; Hirose
2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
Fax:66-48-462-4672)

FEATURES
source
CDS

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BASE COUNT 199 a 148 c 207 g 254 t

ORIGIN

Query Match 20.8%; Score 241.8; DB 3; Length 808;
Best Local Similarity 64.4%; Pred. No. 1.1e-52;
Matches 395; Conservative 0; Mismatches 212; Indels 6; Gaps 2;

QY 555 TGGTTCCACAACTCGTTATTGGGATTGTTGTAAGCTTCTTGACGCTGGCTGGAAAGC 614.
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DB 141 TTCGGTGTCAAAGCCGCTGTGACATATGCAAAAGATGGAACAACTCGAGTGTGAACACG 200
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DB 618 TCCGTCAATATACATTCAACGAAGTGAAGTGTCCAGGTGACTTGCAAGCAAAACCAATG 677
QY 1152 CGAAGAAGTAA 1164
DB 678 CAGAGCCAGTAA 690

RESULT 5
AB045171
LOCUS
DEFINITION

AB045171
Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
cellulase homologue, clone:7-50, complete cds.

AB045171
AB045171.1 GI:8926974
Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
clone:7-50.
Reticulitermes speratus hindgut symbiont 130484
Unclassified.

ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

1. (sites)
Ohtoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
Diverse genes of cellulase homologues of glycosyl hydrolase family
45 from the symbiotic protists in the hindgut of the termite
Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)
21020023
2. (bases 1 to 710)
Ohkuma, M.
Direct Submission
Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
Physical and Chemical Research), Microbiology Laboratory; Hirose
2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
Fax:66-48-462-4672)

FEATURES
source
CDS

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T"

BASE COUNT 185 a 137 c 197 g 191 t

ORIGIN

Query Match 20.7%; Score 240.6; DB 3; Length 710;
Best Local Similarity 64.1%; Pred. No. 2.3e-52;
Matches 398; Conservative 0; Mismatches 214; Indels 9; Gaps 2;

QY 550 GGCAGTGGTTCCAAACTCGTTATTGGGATTGTTGTAAGCTTCTTTCGACGCTGGCTGGA 609
DB 62 GACACGGGAGAACCAACCGCTTATTGGGATTGTTGCAAGCCAGCTGTGCGTGGGAAAA 121
QY 610 AAAGCTTCTGTCACTGCTGCTGTGACACCTGTGCTCCCAATGGTATCTCTTTATTAG-- 667
DB 122 AAAGCTGCTGTACACAGCTGTTGACACTTGTGGAAGAGATGGGACACAGAGTTGCG 181
QY 668 ----ATGCCAATCTCAAGTGGTTGTAACGGTGTGTAATGTTTTCATGTAAACAAC 723
DB 182 AGCAATGACACTGTGAAATCAGCTTGTGATGTTGAGAGAGATATATGTTTATGATCAA 241
QY 724 CAACCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTTCGCTGCTCTCTATTTGCTGGC 783
DB 242 GCACCAATGGGCTGTAAATGACTCTGTGCGTACGCTTTTCTGCTGACGCTGTGCTGGG- 300
QY 784 TCCAAACGAGCTGGATGGTGTGTTGGCTGTGTTATGAATTTGACCTTCTCTCGCGCTGCT 843
DB 301 --GGGCGAAGCGAGCTTGTGCAATTTGCTTATGAGCTTACATTTCAAGAGTGGACAGTG 358
QY 844 TCTGGAAGAAGATGTTGTTTCAAGTTACCAACCGGTGGCGATTTAGGCTCTAACCAAC 903
DB 359 AATGGAAGAAGATGTTGTTTACAGTCAACCAACCGGTGGTGTATGTTGCTGCTGATCAG 418
QY 904 TTTGATTTGCAATGCGCGGTGGTGGCTGTGATCTTCAATGCTGTCTGCTCTCAATGG 963
DB 419 TTTGATCTTGGGATTCGGGTGGAGTGTGGGATCTTACCAACCGGTGGACCCAGCAATCA 478
QY 964 GGCGCTCCCAATGATGGCTGGGAGCTAGATATGTTGGTGTCTGACGCTCTCTCTGACTGT 1023


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RESULT 9
LOCUS AB045166
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
ACCESSION AB045166
VERSION AB045166.1 GI:8926964
KEYWORDS Reticulitermes speratus hindgut symbiont 130484 CDNA to mRNA,
SOURCE Reticulitermes speratus hindgut symbiont 130484
ORGANISM Reticulitermes speratus hindgut symbiont 130484
REFERENCE 1 (bases 1 to 798)
AUTHORS Ohtoko, K., Ohkuma, M., Moriya, S., Inoue, T., Ueami, R. and Kudo, T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family
JOURNAL 45 from the symbiotic protists in the hindgut of the termite
MEDLINE Reticulitermes speratus
EXTREMOPHILES 4 (6), 343-349 (2000)
REFERENCE 2 (bases 1 to 798)
AUTHORS Ohkuma, M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
Physical and Chemical Research), Microbiology Laboratory; Hirotsawa
2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
Fax:66-48-462-4672)
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RN"
BASE COUNT 195 a 154 c 226 g 222 t 1 others
ORIGIN
Query Match 19.6%; Score 227.8; DB 3; Length 798;
Best Local Similarity 62.8%; Pred. No. 5.5e-49;
Matches 390; Conservative 0; Mismatches 222; Indels 9; Gaps 2;
QY 549 TGGCAGTGTTCACAACTCGTTATTGGGATTGTTGTAAGCTTCTTGCAGCTGGCCTCG 608
DB 74 TGACATGGGCAAAACAAACAGGTATTGGGACTCTGCAAGGCGAGTTGTGGCTGGGAAGC 133
QY 609 AAAAGCTTCTGTCACTGGTCTGTGACACCTGTGCTCCAATGGTATCTCTTTATTAG- 667
DB 134 GAAAGCGGAGCTGAGCAAGCCATTGCACATCGCGGAAGACGGGACCAACAGATTGC 193
QY 668 -----ATGCCAATGCTCAAGTGGTTGAACGGTGTGTAATGGTTTCATGTGTAACACAA 722
DB 194 GAGCAACGACACCGTGAAGAGTGGTTGTATGATGCGGGGACGGTTATATGTGCTATGATCA 253
QY 723 CCAACCTCGGCTGCTCAATGATGAGCTCGCTTACGTTTGGCTGCTGCTCTATTGCTCG 782
DB 254 AACCGTGGGGGCTCAACGACTCATACGCCCTTGGGCTTGTGCTGCGACAAATTCAGG 313
QY 783 CTCACACGAGCTGGATGGTGTGGCTGTTATGAATTGACCTTCACTTCTGGGCGCTGC 842
DB 314 CGCGGAGAGGCTG---CTTGCTGCAACTGTTATGATGATGACATTCATCTTCTGGCCCGT 370
QY 843 TTCTGGAAGAAGATGGTTGTTCAAGTTTACCAACACCGGTGGCGAATTAGGCTCTTAACCA 902

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371 TAATGGCAAGAGATGACAGTACAGGTTACCAACACTGGAGCGAGCTTGGGTTCCAATCA 430
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DB 431 ATTGATCTTGAATTCAGGCGCGGTGTGGGCACTTACAATGATGACGCGCTCAGTC 490
QY 963 GGGCGCTCCCAATGATGGCTGGGAGCTAGATATGATGATGATGATGATGATGATG 1022
DB 491 TGGCGCTCTCTGCTGACGGATGGGTAGTCGGTATGGTGAGTTTCTCTCGCAGCAATG 550
QY 1023 TGCTCTCTCTCTCTCTCTCTCTCAAGCTGGTGTGTAATGGAGATTCACATGGTTCAAGAA 1082
DB 551 CTCGCAACTTCTTCAAGTCTTCAAGCTGGCTGCCAGTGGAGATTGATTGGTTCAAAA 610
QY 1083 CTCTGATAACCCCTACATGACCTTCAAGGAGCTTCAAGTGTCTCTCTCTCTCTCTCTCT 1142
DB 611 CGCCGACATCTCGTCTCAATGATTTCAATGTTGGTGTGTCGCCCCAGTGAGTTGTCGAA 670
QY 1143 CTCAGGTTTGGCAAGAAAGTA 1163
DB 671 AACCAATTGCAGACCAATTA 691

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RESULT 10
FSOKCH
LOCUS Fusarium oxysporum k-family cellulase homologue mRNA linear PLN 28-APR-1995
DEFINITION Fusarium oxysporum k-family cellulase homologue mRNA, complete cds.
ACCESSION L29381
VERSION L29381.1 GI:520822
KEYWORDS K-family cellulase homologue; cellulase; homologue.
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
REFERENCE 1 (bases 1 to 1443)
AUTHORS Sheppard, P.O., Grant, F.J., Oort, P.J., Oort, P.J., Sprecher, C.A., Foster, D.C.,
Hagen, F.S., Upshall, A., McKnight, G.L. and O'Hara, P.J.
TITLE The use of conserved cellulase family-specific sequences to clone
JOURNAL cellulase homologue cDNAs from Fusarium oxysporum
MEDLINE Gene 150 (1), 163-167 (1994)
PUBMED 95047531
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source Location/Qualifiers
1..1443
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/db_xref="taxon:5507"
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BASE COUNT 325 a 448 c 332 g 338 t
ORIGIN
Query Match 15.0%; Score 221.4; DB 8; Length 1443;
Best Local Similarity 63.9%; Pred. No. 2.8e-47;
Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;
QY 547 TCTGGCAGTGGTTCACAACTCGTTATTGGGATTGTTGTAAGCTTCTTGCAGCTGGCCT 606
DB 137 TCTGGAAGCGGTCACTCTACTCGATCTGGGATTGCTGCAAGCCCTTCTGCTCTTGGAGC 196
QY 607 GGAAAGACTTCTGTCACTGGTCTCTGTGACACCTGTGCTGCCCTCCAATGGTATCTCTTTATTA 666

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Db      197  GGAAGGCTGCTCAACGCCCTCTTAACCTTGTGATGAAGAACGACCAACCCATTCC 256
QY      667  GATGCCAATGCTCAAGTGGTGTGTA --- CGGTGGTAAATGTTTATGTTGTAACAAAC 723
Db      257  AACACCAATGCTGTCAACGGTGTGAGGGTGTGTTCTGCTTATGCTTTGACCAACTAC 316
QY      724  CAACCTTGGGCTGTCAATGATGAGCTGCTTACGGTTCGCTGCTGCTCTATTGCTGGC 783
Db      317  TCTCCCTGGGCTGTCAACGATGAGCTTGCTACGGTTCGCTGCTCAACGAATCTCCGGT 376
QY      784  TCCACCAAGCTGATGAGTGTGTTGCTGTTATGAATGACCTTCACTTCTGCGCTCTCT 843
Db      377  GGCTCCGAGGCGAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436
QY      844  TCTGGAAGAGATGTTGTTCAAGTTACCAACCGGTGCGATTTAGGCTCTTAACCAAC 903
Db      437  AAGGGCAAGAGATGATGCTCAGTCCACCAACACTGGAGGTGATCTCGGCGACCAAC 496
QY      904  TTTGATTTGCAATGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
Db      497  TTCGATCTCATGATGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
QY      964  GCGCTGCCAATGATGCTGCGGAGCTAGATATGTTGCTGCTGCTGCTGCTGCTGCTG 1023
Db      557  GG-----CAAGGCTCTCGGCGTCCAGTACGGGGTATCTCTCCCGAAGCGAATG 610
QY      1024  GCCTCTCTCCCTCTCTCAAGCTGTTGTAATGGAGATTCAACTGTTCAAGAAC 1083
Db      611  GATAGCTACCCGAGCTTCTCAAGACGGTTCGCCATCTTCCGACGGCTGCACTCTG 670
QY      1084  TCTGATACCTTACCATTGACCTTCAAGGAAGTTACCTGTCC 1124
Db      671  GCCGACACCTGACTTCACTTTGAGCAGGTTCAAGTGCCCC 711

RESULT 11
LOCUS      A21795      1473 bp      mRNA      linear      PAT 20-SEP-1995
DEFINITION F. oxysporum mRNA for endonuclease component.
ACCESSION A21795
VERSION    A21795.1 GI:1246874
KEYWORDS   Fusarium oxysporum.
SOURCE     Fusarium oxysporum.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
FEATURES   Location/Qualifiers
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                CKRDDSSFPFAKVDTSASKQPSSAKKTTSAAQAQPKTKDSAPVQKSSTKPAA
                QPEPTKPADKPTDKPVAATKPAATKVPQVKNPKTTQKVRGTRGSCPAKTATAKA
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BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN
Query Match 19.08; Score 221.4; DB 6; Length 1473;
Best Local Similarity 63.98; Pred. No. 2.8e-47;
Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;
QY      547  TCTGCGAGTGTTCACCACTGTTATGGGATTTGTTGTAAGCTTCTTCCAGCTGGCCT 606

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Db      151  TCTGGAAGCGGTCACTTACTCGATCTGGATTGCTCAAGCCTTCTTGTCTTGGAGC 210
QY      607  GGAAGAGCTTCTGCTCACTGGTCCCTGTGACACCTGCGCTCCCAATGATGATCTCTTTATTA 666
Db      211  GGAAGAGCTGCTGTCAACGCCCTCTGCTTTAACTTTGATGAAGAACGACCAACCCATTCC 270
QY      667  GATGCCAATGCTCAAGTGGTGTGTA --- CGGTGGTAAATGTTTATGTTGTAACAAAC 723
Db      271  AACACCAATGCTGTCAACGGTGTGAGGGTGTGCTGCTGCTTATGCTTTCGACCAACTAC 330
QY      724  CAACCTTGGGCTGTCAATGATGAGCTGCTGCTTACGGTTCGCTGCTGCTCTTATTCCTGGC 783
Db      331  TCTCCCTGGGCTGTCAACGATGAGCTTGCCCTACGGTTCGCTGCTACCAAGATCTCCGGT 390
QY      784  TCCACCAAGCTGGAATGTTGTTGGCTGTTATGAATGACCTTCACTTCTTGGCGCTGCT 843
Db      391  GGCTCCGAGGCGAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450
QY      844  TCTGGAAGAGATGTTGTTCAAGTTACCAACCGGTGCGGATTTAGGCTCTTAACCAAC 903
Db      451  AAGGGCAAGAGATGATGCTCCAGTCCACCAACACTGGAGGTGATCTCGGCGACCAAC 510
QY      904  TTTGATTTGCAATGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
Db      511  TTCGATCTCATGATGCTCGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 570
QY      964  GCGCTCCCAATGATGCTGCGGAGCTAGATATGTTGTTGCTGCTGCTGCTGCTGCTGCT 1023
Db      571  GG-----CAAGGCTCTCGGCGTCCAGTACGGGGTATCTCTCCCGAAGCGAATG 624
QY      1024  GCCTCTCTCCCTCTCTCAAGCTGTTGTAATGGAGATTCAACTGTTCAAGAAC 1083
Db      625  GATAGCTACCCGAGCTTCTCAAGACGGTTCGCCATCTTCCGACGGTTCGATTTGACT 684
QY      1084  TCTGATAACCTTACCATTGACCTTCAAGGAAGTTACCTGTCC 1124
Db      685  GCCGACACCTGACTTCACTTTGAGCAGGTTCAAGTGCCCC 725

RESULT 12
LOCUS      A23637      1473 bp      mRNA      linear      PAT 19-SEP-1995
DEFINITION F. oxysporum endoglucanase gene.
ACCESSION A23637
VERSION    A23637.1 GI:832888
KEYWORDS   endoglucanase.
SOURCE     Fusarium oxysporum.
            Fusarium oxysporum.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE 1 (bases 1 to 1473)
            Convents, A.C., Busch, A. and Baek, A.C.
            Detergent compositions with high activity cellulase and softening
            clays
            Patent: EP 0495258-A 3 22-JUL-1992;
            THE FROCTER & GAMBLE COMPANY
            Location/Qualifiers
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                ALGCAQYGISRSRSCDSYPELLKDGCHWFDNFENADNPDFTFEQVQCPKALLDISG
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BASE COUNT      343 a  453 c  337 g  340 t
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Query Match      19.0%; Score 221.4; DB 6; Length 1473;
Best Local Similarity 63.9%; Pred. No. 2.8e-47;
Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;

QY 547 TCTGGCAGTGTTCACAACTCGTATTGGGATTGTGTAAAGCTTCTTGCAGCTGGCCT 606
DB 151 TCTGGAAGCGGTCACTCTACTCGATTGGATTGCTGCAAGCCTTCTTGTCTTTGGAGC 210
QY 607 GGAAGAGCTTCTGTCTACTGTCTCTGTGACACCTGCTCCCAATGGTATCTTTATTA 666
DB 211 GGAAGAGCTGTCTCAACGCCCTCTTAACTTGTGATAAGAACGACCAACCCATTTC 270
QY 667 GATGCCAATGCTCAAGTGGTTGTAA---CGGTGGTAAATGGTTTCATGTAAACAAC 723
DB 271 AACACCAATGCTCAACGGTTGTGAGGGTGGTGGTTCGTCTATGCTTGCACCACTAC 330
QY 724 CAACCTTGGGCTGTCAATGATGAGCTGCTTACGGTTTCGCTGCTGCTCTTATTTGCTGC 783
DB 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTCGCTGCTACCAAGATCTCCGGT 390
QY 784 TCCACGAGCTGGATGGTGTGCTGCTTATGAATGACCTTCACTTCTGCGGCTGCT 843
DB 391 GGTCTCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450
QY 844 TCTGGAAGAGATGGTGTTCAGAGTTACCAACCGGTGGCGATTAGGCTCTAACCAAC 903
DB 451 AAGGCGAAGAGATGATGCTCAGTCCACCAACACATGGAGGTGATCTCGGCGACACCAAC 510
QY 904 TTGATTTCGAAATGCGCGGTGGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 963
DB 511 TTGATCTCATGATGCCCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 570
QY 964 GCGGCTCCCAATGATGGCTGGGAGCTAGATATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1023
DB 571 GG-----CAAGGCTCTCGGCGGTGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 1024 GCCTCTCTTCTGCTCTTCAAGCTGGTGTGTAATGAGAGATTCAACTGGTTCAGAAC 1083
DB 625 GATAGTACCCCGAGCTTCTCAAGGACGGTTGCCACTGGCGATTGCTGCTGCTGCTGCTGCTGCT 684
QY 1084 TCTGATAACCTTACCATGACCTTCAAGGAAGTTTACCTGTCC 1124
DB 685 GCGGACAACTTCACTTCACTTGTGAGCAGGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725

RESULT 13
A23646
LOCUS      A23646      1473 bp      mRNA      linear      PAT 23-FEB-1995
DEFINITION F. oxysporum endoglucanase gene.
ACCESSION  A23646
VERSION     A23646.1  GI:832892
KEYWORDS
SOURCE
ORGANISM   Fusarium oxysporum.
            Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE  1 (bases 1 to 1473)
AUTHORS   Convents, A.C., Busch, A. and Baek, A.A.
TITLE     Detergent compositions with high activity cellulase and quaternary
            ammonium compounds
JOURNAL   Patent: EP 0495554-A 3 22-JUL-1992;
            THE PROCTER & GAMBLE COMPANY
FEATURES
source     1. 1473
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            /strain="DSM 2672"
            /db_xref="taxon:5507"
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BASE COUNT      343 a  453 c  337 g  340 t
ORIGIN

Query Match      19.0%; Score 221.4; DB 6; Length 1473;
Best Local Similarity 63.9%; Pred. No. 2.8e-47;
Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;

QY 547 TCTGGCAGTGTTCACAACTCGTATTGGGATTGTGTAAAGCTTCTTGCAGCTGGCCT 606
DB 151 TCTGGAAGCGGTCACTCTACTCGATTGGATTGCTGCAAGCCTTCTTGTCTTTGGAGC 210
QY 607 GGAAGAGCTTCTGTCTACTGTCTCTGTGACACCTGCTCCCAATGGTATCTTTATTA 666
DB 211 GGAAGAGCTGTCTCAACGCCCTCTTAACTTGTGATAAGAACGACCAACCCATTTC 270
QY 667 GATGCCAATGCTCAAGTGGTTGTAA---CGGTGGTAAATGGTTTCATGTAAACAAC 723
DB 271 AACACCAATGCTCAACGGTTGTGAGGGTGGTGGTTCGTCTATGCTTGCACCACTAC 330
QY 724 CAACCTTGGGCTGTCAATGATGAGCTGCTTACGGTTTCGCTGCTGCTCTTATTTGCTGC 783
DB 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTCGCTGCTACCAAGATCTCCGGT 390
QY 784 TCCAAAGAGCTGGATGGTGTGCTGCTTATGAATGACCTTCACTTCTGCGGCTGCT 843
DB 391 GGTCTCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450
QY 844 TCTGGAAGAGATGGTGTTCAGTACCACCGGTGGCGATTAGGCTCTAACCAAC 903
DB 451 AAGGCGAAGAGATGATGCTCAGTCCACCAACACATGGAGGTGATCTCGGCGACACCAAC 510
QY 904 TTGATTTCGAAATGCGCGGTGGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 963
DB 511 TTGATCTCATGATGCCCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 570
QY 964 GCGGCTCCCAATGATGGCTGGGAGCTAGATATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1023
DB 571 GG-----CAAGGCTCTCGGCGGTGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 1024 GCCTCTCTTCTGCTCTTCAAGCTGGTGTGTAATGAGAGATTCAACTGGTTCAGAAC 1083
DB 625 GATAGTACCCCGAGCTTCTCAAGGACGGTTGCCACTGGCGATTGCTGCTGCTGCTGCTGCTGCT 684
QY 1084 TCTGATAACCTTACCATGACCTTCAAGGAAGTTTACCTGTCC 1124
DB 685 GCGGACAACTTCACTTCACTTGTGAGCAGGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725

RESULT 14
A23955
LOCUS      A23955      1473 bp      DNA      linear      PAT 01-MAR-1995
DEFINITION Endoglucanase gene.
ACCESSION  A23955
VERSION     A23955.1  GI:832896
KEYWORDS
SOURCE
ORGANISM   Fusarium oxysporum.
            Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE  1 (bases 1 to 1473)
AUTHORS   Baek, A.C., Busch, A. and Ceulemans, R.A.A.
TITLE     Compact detergent compositions with high activity cellulase

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JOURNAL Patent: EP 0495257-A 3 22-JUL-1992;
THE PROCTER & GAMBLE COMPANY
FEATURES Location/Qualifiers
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1. .1473
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BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 19.0%; Score 221.4; DB 6; Length 1473;
Best Local Similarity 63.9%; Pred. No. 2.8e-47;
Matches 371; Conservative 0; Mismatches 201; Indels 9; Gaps 2;
Qy 547 TCTGGCAGTGGTTCACAACTCGTTATGGGATTTGTTAAAGCTTCTTTGACGTGGCCT 606
Db 151 TCTGGAAGCGGTCACTTACTCGATACCTGGGATTTGCTGAAGCCTTCTTGTCTTTGGAGC 210
Qy 607 GGAAGAAGCTTCTGTCACGTGCTGTTGACACCTGTCCTCCAATGGTATCTCTTTATTA 666
Db 211 GGAAGAAGCTTCTGTCACGCGCTGCTTTAACTTGTGATAAGAACGACAAACCCCATTTCC 270
Qy 667 GATGCCAATGCTCAAGTGGTGTAA---CGTGGTAAATGTTTCATGTGTAACAACAAC 723
Db 271 AACCAATGCTGTCAACGCTGTGAGGGTGGTGTCTGCTTATGATAAGAACGACAACTAC 330
Qy 724 CAACCTTGGGCTGTCAATGAGCTGCTTACGTTTTCGCTGCTGCTCTATTGTGGC 783
Db 331 TCTCCCTGGGCTGTCAACGATGAGCTTACGTTTTCGCTGCTGCTTACCAAGATCTCGGT 390
Qy 784 TCCGAAGAAGATGCTTTCAGTTTACCAACCGGTGGGATTTAGCTCTGCTGCTCAATGG 843
Db 451 AAGGCGAAGAAGATGATGTCGCTCCACCACTGGAGGTGATCTCGGCGAACCAAC 510
Qy 904 TTGTGATTGCAATGCGCGGTGGGCTGATCTTCAATGGCTGTGCTGCTCAATGG 963
Db 511 TTGATCTCATGATGCGCGGTGGGCTGATCTTCAAGCGGTGATCTCTCCCGAAGCGAATGT 570
Qy 964 GCGCTGCCAATGATGCTGGGAGCTAGATATGGTGGTGTGAGCTGTGCTCTGACTGT 1023
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RESULT 15
A23959
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DEFINITION Endoglucanase gene.
ACCESSION A23959
VERSION A23959.1 GI:832900
KEYWORDS

SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 1473)
AUTHORS McCorquodale, F. and Busch, A.
TITLE Dye transfer inhibiting compositions
JOURNAL Patent: EP 0540784-A 3 12-MAY-1993;
THE PROCTER & GAMBLE COMPANY
FEATURES Location/Qualifiers
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BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 19.0%; Score 221.4; DB 6; Length 1473;
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Db 151 TCTGGAAGCGGTCACTTACTCGATACCTGGGATTTGCTGAAGCCTTCTTGTCTTTGGAGC 210
Qy 607 GGAAGAAGCTTCTGTCACGTGCTGTTGACACCTGTCCTCCAATGGTATCTCTTTATTA 666
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